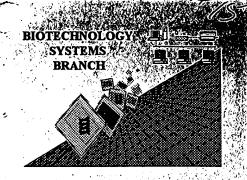
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/586,5940

Art Unit / Team No.

7/23/98

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

	ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 08/586,5940
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces. All text must be visible on page.
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
7	Wrong Designation	Sequence(s) contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
0	Use of N's or Xaa's (NEW RULES)	Use of N's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
1	Use of <213>Organism (NEW RULES)	Sequence(s) are missing this mandatory field or its response.
2	Use of <220>Feature (NEW RULES)	Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
3		File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, Jun 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.
4	OTHER	



PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/586,594C

DATE: 07/23/98 TIME: 09:24:21

INPUT SET: S27599.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

,	SEQUENCE LISTING		
1 2	SEQUENCE LISTING		
3	(1) General Information: (i) APPLICANT: Friedman, Jeffrey M. Lee Gwo-Hua SEQUENCE LISTING MENA Function Firedway Sheet		
4			
5	(i) APPLICANT: Friedman, Jeffrey M.		
6	Lee, Gwo-Hua		
7	Proenca, Ricardo		
8			
9	(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC		
10	ACIDS ENCODING THE RECEPTOR, AND USES THEREOF		
11			
12	(iii) NUMBER OF SEQUENCES: 56		
13			
14	(iv) CORRESPONDENCE ADDRESS:		
15	(A) ADDRESSEE: David A. Jackson, Esq.		
16	(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor		
17 18	(C) CITY: Hackensack		
19	(D) STATE: New Jersey		
20	(E) COUNTRY: USA		
21	(E) CONTRI. OSA (F) ZIP: 07601		
22	(1) 211: 0/001		
23	(V) COMPUTER READABLE FORM:		
24	(A) MEDIUM TYPE: Floppy disk		
25	(B) COMPUTER: IBM PC compatible		
26	(C) OPERATING SYSTEM: PC-DOS/MS-DOS		
27	(D) SOFTWARE: PatentIn Release #1.0, Version #1.30		
28			
29	(vi) CURRENT APPLICATION DATA:		
30	(A) APPLICATION NUMBER: US 08/586,594		
31	(B) FILING DATE:		
32	(C) CLASSIFICATION:		
33			
34	(viii) ATTORNEY/AGENT INFORMATION:		
35	(A) NAME: Jackson Esq., David A.		
36	(B) REGISTRATION NUMBER: 26,742		
37	(C) REFERENCE/DOCKET NUMBER: 600-1-162		
38	(in) MRIEGONAUNICAMION INFORMATION.		
39	(ix) TELECOMMUNICATION INFORMATION:		
40 41	(A) TELEPHONE: 201-487-5800		
41	(B) TELEFAX: 201-343-1684		
42			

43

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/08/586,594C

DATE: 07/23/98 TIME: 09:24:23

INPUT SET: S27599.raw

71 TTGCTTTGGG 120	99.raw
46 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2529 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 51 52 (ii) MOLECULE TYPE: CDNA 53 54 (iii) HYPOTHETICAL: NO 55 60 (iv) ANTI-SENSE: NO 57 58 60 (vi) IMMEDIATE SOURCE: 60 (B) CLONE: A15 (OB-Ra) 61 62 63 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 GGGCTCTGG 60 67 68 69 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG 71 72 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA 73 GACACTGCT 74 75 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT 76 AGAGTCCTG 77 78 ATGAAAAGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA 79 GACCCCTTC 300 81 AAGAATATAG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT 82 AGATGATCG 360 87 TGTGAATTGC 360 88 CCCTTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG 87 TGTGAATTTA ACTCCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTCTC 88 GATTATTTT 89 GAAATCACAT CTGCCGGTA ACCCAGAGCC AAACTCAACT ACGCTCTTCT 60 GAAATCACAT CTGCCGGTT ACCCAGAGCC AAACTCAACT ACGCTCTTCT 50 GAAATCACAT CTGCCGGTTA ACCCAGAGCC AAACTCAACT ACGCTCTTCT 51 GCCCATGCTT 520 53 GTTGTAAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA 54 TGGTAAATTA 57 TGGTAAATTA 58 GATCTATTT 59 GAAATCACAT CTGCCGGTTA ACCCAGAGCC AAACTCAACT ACGCTCTTCT 59 GAAATCACAT CTGCCGGTTA ACCCAGAGCC AAACTCAACT ACGCTCTTCT 540 551 552 553 554 555 556 557 557 557 557 558 559 (vii) IMMEDIATE SOURCE: 60 AAGACTACACC CTTAAGGTTTCAG ACTGTCCAAT ACGCTCTTCT 63 GGCCATGCTT 640 651 652 653 654 (vii) SEQUENCE DESCRIPTION: SEQ ID NO:1: 665 67 67 686 697 697 697 697 697	
-> 47 (A) LERGTH: 2529 base pairs (B) Type: nucleic acid 49 (C) STRANDEDNESS: double (D) TOPOLOGY: linear 51 52 (ii) MOLECULE TYPE: CDNA SALA JULY, AND 53 (iii) HYPOTHETICAL: NO 55 (iv) ANTI-SENSE: NO (N) IMMEDIATE SOURCE: (B) CLONE: Al5 (OB-Ra) 61 62 63 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 68 69 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG 70 71 72 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA 73 GACACTGCCT 74 75 76 77 78 ATGAAAGGGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT 77 78 ATGAAAGGGA AGCTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA 80 81 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT 82 AAGAATTATG ACTCTAAGAG CCAGTTTTTA TATGATCTGC CTGAAGTCAT 83 84 CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG 85 TCTTCGGGGA 87 TGTGAATTTG AGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTCT 88 GAGTTATTTG 480 90 GAAATCACAT CTGCCGGTT GAGTTTTCAG TCACCTCTGA TGTCACTCCA 89 GAAATCACAT CTGCCGGTT GAGTTTTCAG TCACCTCTGA TGTCACTCCA 89 GAAATTATTC ATGTGCCGGT ACCCAGAGGC AAACTCAACT ACGCTCTTCT 50 GAGATTATTT 50 GAAATCACAT CTGCCGGTT GAGTTTTCAG TCACCTCTGA TGTCACTGCA 91 GCCCATGCTT 540 93 GTTGTGAAACC GAGTTATTTA 600	
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61 62 63 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA 67 GGCGCTCTCG 60 69 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG 71 72 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA 73 GACACTGGCT 74 75 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT 76 AGAGTGCTGG 77 78 ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA 680 81 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT 82 AGATGATTCG 83 84 CCCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG 85 TCTTCGGGGA 86 87 TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT 88 GATGTATTT 89 90 GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA 91 GCCCATGCTT 92 93 GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA 94 TGGTAATTTA 600	reacc
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61 62 63 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA 67 GGCGCTCTCG 60 69 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG 71 72 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA 73 GACACTGGCT 74 75 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT 76 AGAGTGCTGG 77 78 ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA 680 81 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT 82 AGATGATTCG 83 84 CCCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG 85 TCTTCGGGGA 86 87 TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT 88 GATGTATTT 89 90 GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA 91 GCCCATGCTT 92 93 GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA 94 TGGTAATTTA 600	_
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> 66 GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA 68 69 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG> 70 TTGCTTTGGG 120 71 72 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA 73 GACACTGGCT 180 74 75 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT 77 78 ATGAAAGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA 79 GAACCCCTTC 300 81 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT 82 AGATGATTCG 360 83 84 CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG 86 87 TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT 88 GATGTATTTG 480 89 90 GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCGA TGTCACTGCA 91 GCCCATGCTT 540 92 93 GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA> 94 TGGTAATTA 600	
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